

# RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/600,997A  
Source: IFW/J6  
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IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/600,997A

DATE: 09/28/2006

TIME: 09:05:34

Input Set : A:\A-71608 (substitute).ST25.txt  
 Output Set: N:\CRF4\09282006\J600997A.raw

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3 <110> APPLICANT: Murphy, Kenneth
4      Watanabe, Norihiko
5      Murphy, Theresa
6      Yang, Jianfei
8 <120> TITLE OF INVENTION: BTLA Nucleic Acids (amended)
10 <130> FILE REFERENCE: A-71608
12 <140> CURRENT APPLICATION NUMBER: 10/600,997A
13 <141> CURRENT FILING DATE: 2003-06-20
15 <150> PRIOR APPLICATION NUMBER: US 60/390,653
16 <151> PRIOR FILING DATE: 2002-06-20
18 <150> PRIOR APPLICATION NUMBER: US 60/438,593
19 <151> PRIOR FILING DATE: 2003-01-06
21 <160> NUMBER OF SEQ ID NOS: 62
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 283
27 <212> TYPE: PRT
28 <213> ORGANISM: Mus musculus
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37 20          25          30
40 Gly Lys His Phe Ile Thr Val Thr Phe Thr Ser Ala Gly Asn Ile
41 35          40          45
44 Gly Glu Asp Gly Thr Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu
45 50          55          60
48 Asn Gly Ile Val Ile Gln Trp Leu Lys Glu Gly Ile Lys Gly Leu Val
49 65          70          75          80
52 His Glu Phe Lys Glu Gly Lys Asp Asp Leu Ser Gln Gln His Glu Met
53 85          90          95
56 Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Val Val Gly Asn
57 100         105         110
60 Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr
61 115         120         125
64 Thr Cys Tyr Ile Arg Thr Ser Lys Gly Lys Asn Ala Asn Leu Glu
65 130         135         140
68 Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Ile Asn Val Asp Tyr Asn
69 145         150         155         160
72 Ala Ser Ser Glu Ser Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln
73 165         170         175
76 Pro Thr Val Ala Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser
77 180         185         190

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 81 195 200 205  
 84 Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser  
 85 210 215 220  
 88 Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val  
 89 225 230 235 240  
 92 Thr Asp Ser Glu Val Lys Arg Arg Ser Gln Leu Gln Leu Leu Asn Ser  
 93 245 250 255  
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 116 20 25 30  
 119 Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala Gly Asn Ile  
 120 35 40 45  
 123 Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro Asp Ile Lys Leu  
 124 50 55 60  
 127 Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly Val Leu Gly Leu Val  
 128 65 70 75 80  
 131 His Glu Phe Lys Glu Gly Lys Asp Glu Leu Ser Glu Gln Asp Glu Met  
 132 85 90 95  
 135 Phe Arg Gly Arg Thr Ala Val Phe Ala Asp Gln Val Ile Val Gly Asn  
 136 100 105 110  
 139 Ala Ser Leu Arg Leu Lys Asn Val Gln Leu Thr Asp Ala Gly Thr Tyr  
 140 115 120 125  
 143 Lys Cys Tyr Ile Ile Thr Ser Lys Gly Lys Gly Asn Ala Asn Leu Glu  
 144 130 135 140  
 147 Tyr Lys Thr Gly Ala Phe Ser Met Pro Glu Val Asn Val Asp Tyr Asn  
 148 145 150 155 160  
 151 Ala Ser Ser Glu Thr Leu Arg Cys Glu Ala Pro Arg Trp Phe Pro Gln  
 152 165 170 175  
 155 Pro Thr Val Val Trp Ala Ser Gln Val Asp Gln Gly Ala Asn Phe Ser  
 156 180 185 190  
 159 Glu Val Ser Asn Thr Ser Phe Glu Leu Asn Ser Glu Asn Val Thr Met  
 160 195 200 205  
 163 Lys Val Val Ser Val Leu Tyr Asn Val Thr Ile Asn Asn Thr Tyr Ser  
 164 210 215 220  
 167 Cys Met Ile Glu Asn Asp Ile Ala Lys Ala Thr Gly Asp Ile Lys Val  
 168 225 230 235 240  
 171 Thr Glu Ser Glu Ile Lys Arg Arg Ser His Leu Gln Leu Leu Asn Ser  
 172 245 250 255

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 186 <213> ORGANISM: Mus musculus  
 188 <400> SEQUENCE: 3  
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 193 accttcaccc tggctggaaa cattggagag gacgggaccc tgagctgcac ttttaaacct 180  
 195 gacatcaaacc tcaacggcat cgtcatccag tggctgaaag aaggcatcaa aggttggtc 240  
 197 cacgagttca aagaaggcaa agacgaccc tcacagcagc atgagatgtt cagaggccgc 300  
 199 acagcagtgt ttgctgatca ggtggtagtt ggcaatgctt ccctgagact gaaaaacgtg 360  
 201 cagctcacgg atgctggcac ctacacatgt tacatccgca cctcaaaagg caaagggaat 420  
 203 gcaaaacctag agtataagac cggagccctc agtatgccag agataaatgt ggactataat 480  
 205 gccaggccatc agagtttacg ctgcggaggtt cctcggtgg tccccccagcc cacagtggcc 540  
 207 tgggcatctc aagtgcacca aggagccaa ttctcagaag tctcgaacac cagctttgag 600  
 209 ttgaactctg agaatgtgac catgaagggtc gtatctgtgc tctacaatgt cacaatcaac 660  
 211 aacacataact cctgtatgtat tgaaaaatgac attgccaag ccactgggaa catcaaagtg 720  
 213 acagattcag aggtcaaaaag gcggagtcag ctgcagctgc tcaactccgg gccttccccg 780  
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 230 actgtcgccct cagctggaa cattggggag gatgaatcc tgagctgcac ttttaaacct 180  
 232 gacatcaaacc ttctgtatcat cgtgatacaa tggctgaagg aagggtttt aggttggtc 240  
 234 catgagttca aagaaggcaa agatgagctg tcggagcagg ataaaaatgtt cagaggccgg 300  
 236 acagcagtgt ttgctgatca agtgcataatgtt ggcaatgctt cttcgcgct gaaaaacgtg 360  
 238 caactcacag atgctggcac ctacaaatgt tataatcatca cttctaaagg caagggaaat 420  
 240 gctaaccctt agtataaaaac tggagccctc agcatccgg aagtgaatgt ggactataat 480  
 242 gccagctcag agacccctgcg gtgtgaggtt ccccgatgg tccccccagcc cacagtggc 540  
 244 tgggcatccc aagtgcacca gggagccaa ttctcggaaag tctccaatac cagctttgag 600  
 246 ctgaactctg agaatgtgac catgaagggtt gtgtctgtgc tctacaatgt tacatcaac 660  
 248 aacacataact cctgtatgtat tgaaaaatgac attgccaag caacaggaa tatcaaagtg 720  
 250 acagaatccgg agatcaaaaag gcggagtcac ctacagctgc taaaactcaaa ggcttctctg 780  
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 257 <210> SEQ ID NO: 5  
 258 <211> LENGTH: 306  
 259 <212> TYPE: PRT  
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 262 <400> SEQUENCE: 5

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264 Met Lys Thr Val Pro Ala Met Leu Gly Thr Pro Arg Leu Phe Arg Glu
265 1 5 10 15
268 Phe Phe Ile Leu His Leu Gly Leu Trp Ser Ile Leu Cys Glu Lys Ala
269 20 25 30
272 Thr Lys Arg Asn Asp Glu Glu Cys Glu Val Gln Leu Asn Ile Lys Arg
273 35 40 45
276 Asn Ser Lys His Ser Ala Trp Thr Gly Glu Leu Phe Lys Ile Glu Cys
277 50 55 60
280 Pro Val Lys Tyr Cys Val His Arg Pro Asn Val Thr Trp Cys Lys His
281 65 70 75 80
284 Asn Gly Thr Ile Trp Val Pro Leu Glu Val Gly Pro Gln Leu Tyr Thr
285 85 90 95
288 Ser Trp Glu Glu Asn Arg Ser Val Pro Val Phe Val Leu His Phe Lys
289 100 105 110
292 Pro Ile His Leu Ser Asp Asn Gly Ser Tyr Ser Cys Ser Thr Asn Phe
293 115 120 125
296 Asn Ser Gln Val Ile Asn Ser His Ser Val Thr Ile His Val Arg Glu
297 130 135 140
300 Arg Thr Gln Asn Ser Ser Glu His Pro Leu Ile Thr Val Ser Asp Ile
301 145 150 155 160
304 Pro Asp Ala Thr Asn Ala Ser Gly Pro Ser Thr Met Glu Glu Arg Pro
305 165 170 175
308 Gly Arg Thr Trp Leu Leu Tyr Thr Leu Leu Pro Leu Gly Ala Leu Leu
309 180 185 190
312 Leu Leu Leu Ala Cys Val Cys Leu Leu Cys Phe Leu Lys Arg Ile Gln
313 195 200 205
316 Gly Lys Glu Lys Lys Pro Ser Asp Leu Ala Gly Arg Asp Thr Asn Leu
317 210 215 220
320 Val Asp Ile Pro Ala Ser Ser Arg Thr Asn His Gln Ala Leu Pro Ser
321 225 230 235 240
324 Gly Thr Gly Ile Tyr Asp Asn Asp Pro Trp Ser Ser Met Gln Asp Glu
325 245 250 255
328 Ser Glu Leu Thr Ile Ser Leu Gln Ser Glu Arg Asn Asn Gln Gly Ile
329 260 265 270
332 Val Tyr Ala Ser Leu Asn His Cys Val Ile Gly Arg Asn Pro Arg Gln
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345 <211> LENGTH: 289
346 <212> TYPE: PRT
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355 Phe Phe Leu Ile Pro Tyr Leu Asp Ile Trp Asn Ile His Gly Lys Glu
356 20 25 30

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359 Ser Cys Asp Val Gln Leu Tyr Ile Lys Arg Gln Ser Glu His Ser Ile  
 360 35 40 45  
 363 Leu Ala Gly Asp Pro Phe Glu Leu Glu Cys Pro Val Lys Tyr Cys Ala  
 364 50 55 60  
 367 Asn Arg Pro His Val Thr Trp Cys Lys Leu Asn Gly Thr Thr Cys Val  
 368 65 70 75 80  
 371 Lys Leu Glu Asp Arg Gln Thr Ser Trp Lys Glu Glu Lys Asn Ile Ser  
 372 85 90 95  
 375 Phe Phe Ile Leu His Phe Glu Pro Val Leu Pro Asn Asn Gly Ser  
 376 100 105 110  
 379 Tyr Arg Cys Ser Ala Asn Phe Gln Ser Asn Leu Ile Glu Ser His Ser  
 380 115 120 125  
 383 Thr Thr Leu Tyr Val Thr Asp Val Lys Ser Ala Ser Glu Arg Pro Ser  
 384 130 135 140  
 387 Lys Asp Glu Met Ala Ser Arg Pro Trp Leu Leu Tyr Ser Leu Leu Pro  
 388 145 150 155 160  
 391 Leu Gly Gly Leu Pro Leu Leu Ile Thr Thr Cys Phe Cys Leu Phe Cys  
 392 165 170 175  
 395 Cys Leu Arg Arg His Gln Gly Lys Gln Asn Glu Leu Ser Asp Thr Ala  
 396 180 185 190  
 399 Gly Arg Glu Ile Asn Leu Val Asp Ala His Leu Lys Ser Glu Gln Thr  
 400 195 200 205  
 403 Glu Ala Ser Thr Arg Gln Asn Ser Gln Val Leu Leu Ser Glu Thr Gly  
 404 210 215 220  
 407 Ile Tyr Asp Asn Asp Pro Asp Leu Cys Phe Arg Met Gln Glu Gly Ser  
 408 225 230 235 240  
 411 Glu Val Tyr Ser Asn Pro Cys Leu Glu Glu Asn Lys Pro Gly Ile Val  
 412 245 250 255  
 415 Tyr Ala Ser Leu Asn His Ser Val Ile Gly Leu Asn Ser Arg Leu Ala  
 416 260 265 270  
 419 Arg Asn Val Lys Glu Ala Pro Thr Glu Tyr Ala Ser Ile Cys Val Arg  
 420 275 280 285  
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 428 <211> LENGTH: 870  
 429 <212> TYPE: DNA  
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 432 <400> SEQUENCE: 7  
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 437 aagagacaat ctgaacactc catcttagca ggagatccct ttgaactaga atgccctgtg 180  
 439 aaatactgtg ctaacaggcc tcatgtgact tggtgcaagc tcaatggAAC aacatgtgt 240  
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 443 cattttgaac caatgctcc taatgacaat gggcataacc gctgttctgc aaattttcag 360  
 445 totaatctca ttgaaaagcca ctcaacaact ctatgtga cagatgtaaa aggtgcctca 420  
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 451 caccaggaa agcaaaatga actctctgac acagcaggaa gggaaatcaa tctgggttat 600  
 453 gtcacacctta agagcgagca aacagaagca agcaccaggc aaaattccca agtactgcta 660

**VERIFICATION SUMMARY**

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